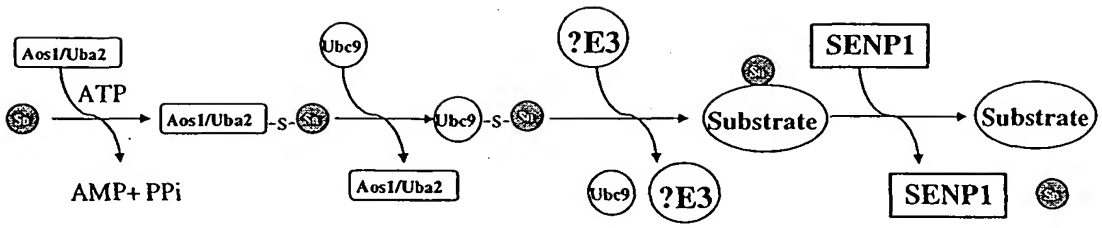



**FIG. 1.** Sentrinization and de-sentrinization pathway.

# FIG. 2

```
1       acctagcgactcttccggtgctgtgaaggcggttccggttcgcggcggttcccgggtttt
61      gcgttccgcgcccggccggaaaccccttcgcatggcagccggttccggttcggactttgt
121     atctttgctaaagtcagtgatgtgaaaagacttgaaatggatgatattgctgataggatg
                                          M  D  D  I  A  D  R  M      8
181     aggatggatgctggagaagtgactttagtgaaccacaactccgtattcaaaacccacctc
        R  M  D  A  G  E  V  T  L  V  N  H  N  S  V  F  K  T  H  L     28
241     ctgccacaaacaggttttccagaggaccagctttcgctttctgaccagcagattttatct
        L  P  Q  T  G  F  P  E  D  Q  L  S  L  S  D  Q  Q  I  L  S     48
301     tccaggcaaggacatttggaccgatcttttacatgttccacaagaagtgcagcttataat
        S  R  Q  G  H  L  D  R  S  F  T  C  S  T  R  S  A  A  Y  N     68
361     ccaagctattactcagataatccttcctcagacagttttcttggctcaggcgatttaaga
        P  S  Y  Y  S  D  N  P  S  S  D  S  F  L  G  S  G  D  L  R     88
421     acctttggccagagtgcaaatggccaatggagaaattctaccccatcgtcaagctcatct
        T  F  G  Q  S  A  N  G  Q  W  R  N  S  T  P  S  S  S  S  S    108
481     ttacaaaaatcaagaaacagccgaagtctttacctcgaaacccgaaagacctcaagtgga
        L  Q  K  S  R  N  S  R  S  L  Y  L  E  T  R  K  T  S  S  G    128
541     ttatcaaacagttttgcgggaaagtcaaaccatcactgccatgtatctgcatatgaaaaa
        L  S  N  S  F  A  G  K  S  N  H  H  C  H  V  S  A  Y  E  K    148
601     tcttttcctattaaacctgttccaagtccatcttggagtggttcatgtcgtcgaagtctt
        S  F  P  I  K  P  V  P  S  P  S  W  S  G  S  C  R  R  S  L    168
661     ttgagccccaagaaaactcagaggcgacatgttagtacagcagaagagacagttcaagaa
        L  S  P  K  K  T  Q  R  R  H  V  S  T  A  E  E  T  V  Q  E    188
721     gaagaaagagagatttacagacagctgctacagatggtcacagggaaacagtttactata
        E  E  R  E  I  Y  R  Q  L  L  Q  M  V  T  G  K  Q  F  T  I    208
781     gccaaacccaccacacatttccttttacacctgtctcgatgtcttagttccagtaaaaat
        A  K  P  T  T  H  F  P  L  H  L  S  R  C  L  S  S  S  K  N    228
841     actttgaaagactcactgtttaaaaatggaaactcttgtgcatctcagatcattggctct
        T  L  K  D  S  L  F  K  N  G  N  S  C  A  S  Q  I  I  G  S    248
901     gatacttcatcatctggatctgccagcattttaactaaccaggaacagctgtcccacagt
        D  T  S  S  S  G  S  A  S  I  L  T  N  Q  E  Q  L  S  H  S    268
961     gtatattccctatcttcttataccccagatgttgcatttggatccaaagattctggtact
        V  Y  S  L  S  S  Y  T  P  D  V  A  F  G  S  K  D  S  G  T    288
1021    cttcatcatccccatcatcaccactctgttccacatcagccagataacttagcagcttca
        L  H  H  P  H  H  H  H  S  V  P  H  Q  P  D  N  L  A  A  S    308
1081    aatacacaatctgaaggatcagactctgtgattttactgaaagtgaaagattcccagact
        N  T  Q  S  E  G  S  D  S  V  I  L  L  K  V  K  D  S  Q  T    328
1141    ccaactcccagttctactttcttccaggcagagctgtggatcaaagaattaactagtgtt
        P  T  P  S  S  T  F  F  Q  A  E  L  W  I  K  E  L  T  S  V    348
1201    tatgattctcgagcacgagaaagattgcgccagattgaagaacagaaggcattggcctta
        Y  D  S  R  A  R  E  R  L  R  Q  I  E  E  Q  K  A  L  A  L    368
1261    cagcttcaaaaccagagattgcaggagcgggaacattcagtacatgattcagtagaacta
        Q  L  Q  N  Q  R  L  Q  E  R  E  H  S  V  H  D  S  V  E  L    388
1321    catcttcgtgtacctcttgaaaaggagattcctgttactgttgtccaagaaacacaaaaa
        H  L  R  V  P  L  E  K  E  I  P  V  T  V  V  Q  E  T  Q  K    408
1381    aaaggtcataaattaactgatagtgaagatgaatttcctgaaattacagaggaaatggag
        K  G  H  K  L  T  D  S  E  D  E  F  P  E  I  T  E  E  M  E    428
1441    aaagaaataaagaatgtatttcgtaatgggaatcaggatgaagttctcagtgaagcattt
        K  E  I  K  N  V  F  R  N  G  N  Q  D  E  V  L  S  E  A  F    448
1501    cgcctgaccattacacgcaaagatattcaaactctaaaccatctgaattggctcaatgat
        R  L  T  I  T  R  K  D  I  Q  T  L  N  H  L  N  W  L  N  D    468
1561    gagatcatcaatttctacatgaatatgctgatggagcgaagtaaagagaagggcttgcca
        E  I  I  N  F  Y  M  N  M  L  M  E  R  S  K  E  K  G  L  P    488
1621    agtgtgcatgcatttaatacctttttcttcactaaattaaaaacggctggttatcaggca
        S  V  H  A  F  N  T  F  F  F  T  K  L  K  T  A  G  Y  Q  A    508
1681    gtgaaacgttggacaaagaaagtagatgtatttctgttgacattcttttggtgcccatt
        V  K  R  W  T  K  K  V  D  V  F  S  V  D  I  L  L  V  P  I    528
1741    cacctgggagtacactggtgtctagctgttgtggactttagaaagaagaatattacctat
        H  L  G  V  H  W  C  L  A  V  V  D  F  R  K  K  N  I  T  Y    548
1801    tacgactccatgggtgggataaacaatgaagcctgcagaatactcttgcaatacctaaag
        Y  D  S  M  G  G  I  N  N  E  A  C  R  I  L  L  Q  Y  L  K    568
1861    caagaaagcattgacaagaaaaggaaagagtttgacaccaatggctggcagcttttcagc
        Q  E  S  I  D  K  K  R  K  E  F  D  T  N  G  W  Q  L  F  S    588
1921    aagaaaagccagattcctcagcagatgaatggaagtgactgtgggatgtttgcctgcaaa
        K  K  S  Q  I  P  Q  Q  M  N  G  S  D  C  G  M  F  A  C  K    608
1981    tatgctgactgtattaccaaagacagaccaatcaacttcacacagcaacacatgccatac
        Y  A  D  C  I  T  K  D  R  P  I  N  F  T  Q  Q  H  M  P  Y    628
2041    ttccggaagcggatggtctgggagatcctccaccgaaaactcttgtgaagactgtctcac
        F  R  K  R  M  V  W  E  I  L  H  R  K  L  L  *                643
2101    ttagcagaccttgaccatgtgggggaccagctctttgttgtctacagccagagaccttgg
2161    aaacagctgctcccagccctctgctgttgtaacaccttgatcctggaccaggccctggc
2221    gagatgcattcacaagcacatctgcctttcctttttgtatctcagatactatttttgcaaa
2281    gaaactttggtgctgtgaaaggggtgagggacatccctaagctgaagagagagactgctt
2341    ttcacttcttcagttctgccatcttgttttcaaagggctccagcctcactcagtccctaa
```

2401 ttatgggactgagaaaagcttggaaagaatcttggtttcatataaattcttgtggttagg
2461 Ccttactaagaagtaggaaagggcatgggcaaaaggtagggataaaaaccac

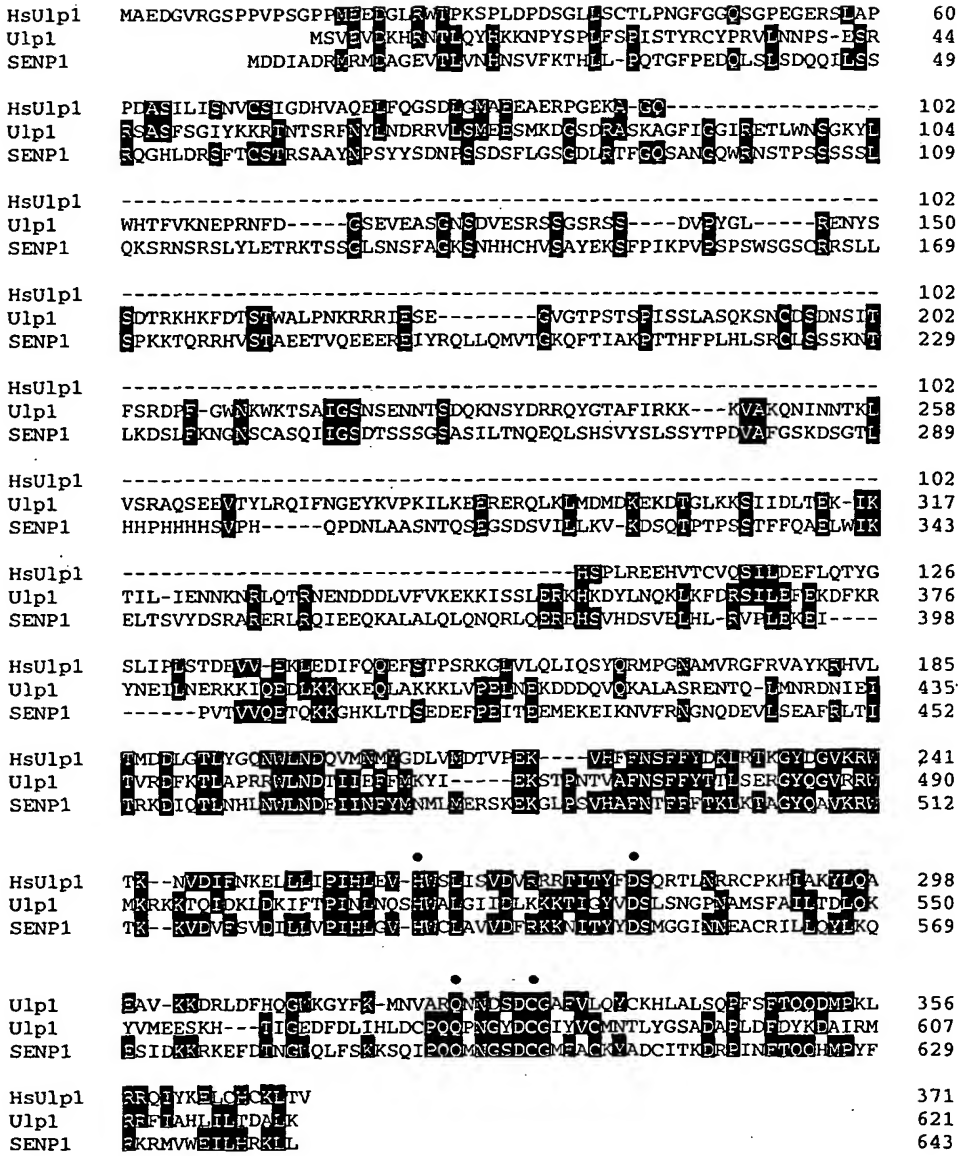



FIG. 3

FIG. 4A.

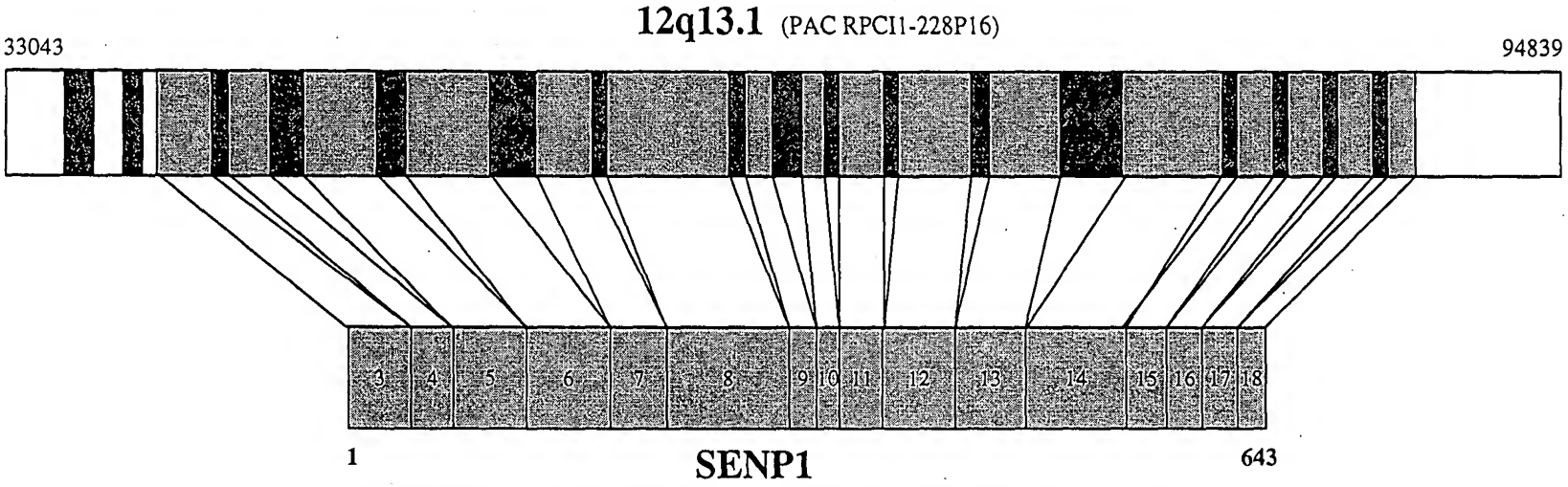
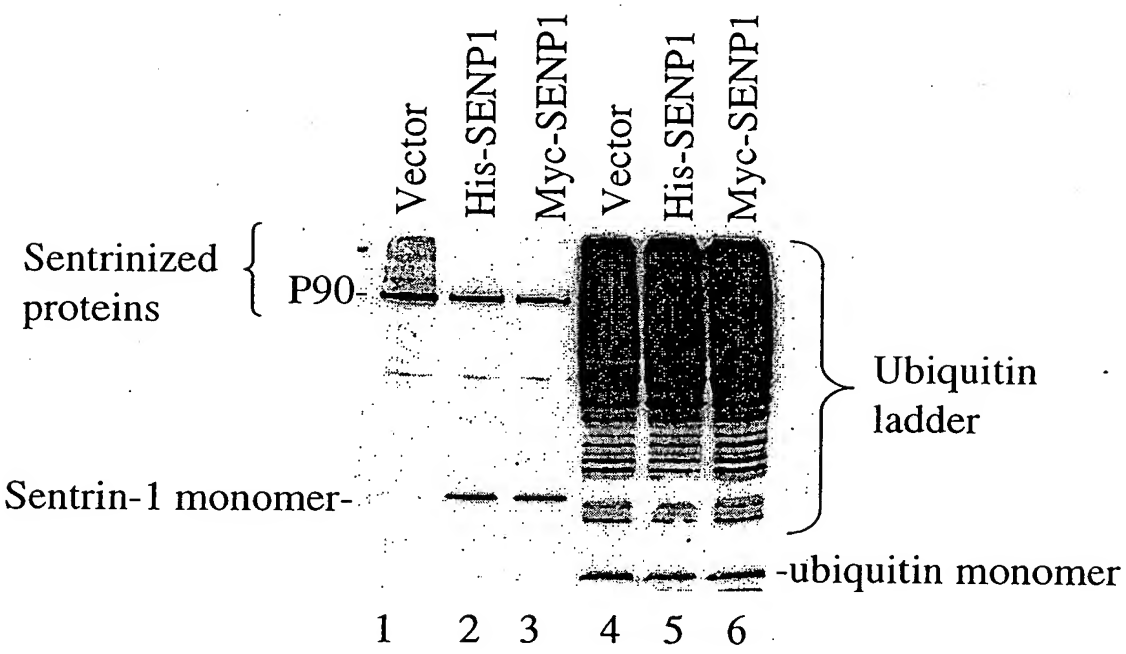


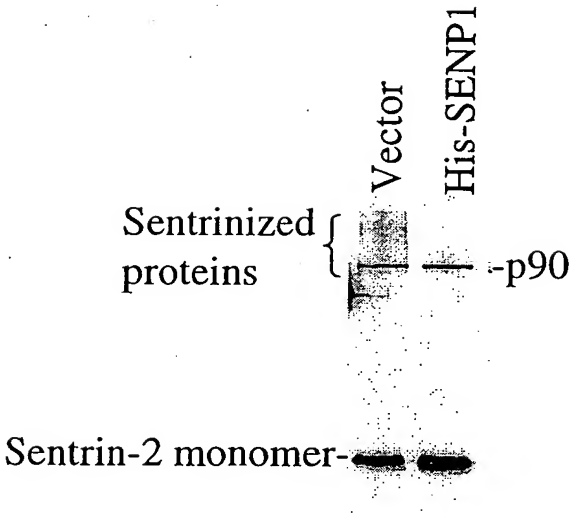

FIG. 4B.

| EXON No. | Length (bp) | 5'Splice donor | Intron length(kb) | 3'Splice acceptor |
|---|---|---|---|---|
| 1 | 112 | GGTTCG GTGAGT | 4.4 | TTATAG GACTTT |
| 2 | 47 | AAATGG GTAAGA | 3.4 | CCCCAG ATGATA |
| 3 | 132 | CAGCAG GTTAGG | 1.5 | GTTTAG ATTTTA |
| 4 | 85 | ACTCAG GTATGA | 7.3 | TTTTAG ATAATC |
| 5 | 160 | CTCAAG GTTCGT | 5.0 | TTTTAG TGGATT |
| 6 | 172 | GAAGAG GTAAGG | 8.7 | TTATAG ACAGTT |
| 7 | 104 | ACACCT GTGAGT | 0.08 | TGCTAG GTCTCG |
| 8 | 284 | CTGAAG GTAAAC | 2.6 | TCTTAG GATCAG |
| 9 | 55 | TCCCAG GTAAAC | 4.7 | CCATAG TTCTAC |
| 10 | 39 | AGAATT GTAAGT | 1.2 | TTCTAG AACTAG |
| 11 | 85 | AACCAG GTAAAA | 0.37 | TTTCAG AGATTG |
| 12 | 156 | ACAGAG GTAAGT | 1.2 | CTCAAG GAAATG |
| 13 | 132 | GATGAG GTAATG | 14.4 | CCACAG ATCATC |
| 14 | 204 | AGCTGT GTGAGT | 0.84 | TCTCAG GTTGTG |
| 15 | 80 | ACTCTT GTAAGT | 0.94 | CTTTAG GCAATA |
| 16 | 85 | AGCCAG GTACCT | 0.53 | CAGGAG ATTCCT |
| 17 | 93 | ACACAG GTGAGC | 0.97 | CTACAG CAACAC |
| 18 | 487 | | | |

# Fig. 5A


Vector
His-SENP1
Myc-SENP1
Vector
His-SENP1
Myc-SENP1
Sentrinized proteins
P90-
Ubiquitin ladder
Sentrin-1 monomer-
-ubiquitin monomer
1 2 3 4 5 6

# Fig. 5B


Vector
His-SENP1
Sentrinized proteins
-p90
Sentrin-2 monomer-